

Cys Gin Gin Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
 180 185 190
 Asn Glu Arg Arg Val Cys Glu Cys Pro Asp Gly Phe Tyr Gly Pro His
 195 200 205
 Cys Glu Lys Ala Leu Cys Ile Pro Arg Cys Met Asn Gly Gly Leu Cys
 210 215 220
 Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
 225 230 235 240
 Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
 245 250 255
 Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
 260 265 270
 Cys Glu Leu Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
 275 280 285
 Ile Gly Lys Ser Lys Cys Lys Cys Pro Lys Gly Tyr Gln Gly Asp Leu
 290 295 300
 Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
 305 310 315 320
 His Glu Pro Asn Lys Cys Gln Cys Arg Glu Gly Trp His Gly Arg His
 325 330 335
 Cys Asn Lys Arg Tyr Gly Ala Ser Leu Met His Ala Pro Arg Pro Ala
 340 345 350
 Gly Ala Gly Leu Glu Arg His Thr Pro Ser Leu Lys Ala Glu Asp
 355 360 365
 Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
 370 375

<210> 3
<211> 1140
<212> DNA
<213> Homo sapiens

<400> 3
atggcccgaa ggagcgcctt cccggccccc ggcgttcggc tctggaggcat cctcttggtc 60
ctgtctggcat tgcggggcggg ggcggggccg cggcaggagg agagcttgta ctatggatc 120
gttgtctacc aggcaaggt actctatggc ttggaaaggat atatctgtat tgtttcagag 180
ggaaaaatgg cacctttatc acatggattc agaaaaggccg aacagagaat gccagcttt 240
cttgtcaata tcattttatc gaattttacc tggcaactcg cggggcggc agatacttc 300
tatgtatcc tgccttgcg ctccctggat aaaggcatca tggcagatcc accgtcaat 360
gtcccttcgc tgggaacagt ggcctacaatg gcatcaggat ttcaggatgg ttcccatgt 420
cttggaaacac aggatgggggt ggcgcattt gaatggatg tgattttat gaatctgaa 480
ggccaaacacca tttccaaac acatcttttctt gctatctttt ttaaaacatg ttcataaagct 540
ggttggcccg gtgggtggcg aaatggggcc ttttgtaatg aaagacccat tgcggatgtl 600
ccgtatgggt tccacggacc tcacttgttag aaagccccctt gtacccccc acgtatgtat 660
gttggacttt tggttgcctt tgggttcgc atctgcctat ctggatcttta tggagtgtat 720
ttgtgacaaac caaatgtgc tttatggatg ggacccgtttt ctacccctgg 780
aaatgtatcc ggcctccagg actatggggaa gaggatgtt aaatcggaa atgcccacaa 840
ccctgtcgaa tttggggatcc atgcatttgtt aaatgcataat gtaatgttcc caaagggttt 900
cggggagacc tttgttccaa ggcgtgtgc gaggctgtt atgggtgcaca tggaaacctgc 960
catgaaccca acaaatggcc atgtcaagaa gtttggatgtt gaaatggatgtt caataaaaagg 1020
tacggaaatca tgccttgggg ccaggcaggccg cccatgttccatg gcaatccacccg 1080
cttcactta taatggccgg ggggggggg gatccactgtt aatccatata catctgttca 1140

<210> 4
<211> 378
<212> PRT
<213> Homo sapiens

<400> 4
Met Ala Arg Arg Ser Ala Phe Pro Ala Ala Leu Trp Leu Trp Ser
 1 5 10 15
 Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro Pro Gln
 20 25 30

Glu-Glu Ser-Leu Tyr Leu Trp Ile-Asp Ala His Gln Ala Arg Val Leu
 35 40 45
 Ile-Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
 50 55 60
 Pro Phe-Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
 65 70 75 80
 Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
 85 90 95
 Ala-Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
 100 105 110
 Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
 115 120 125
 His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
 130 135 140
 Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu
 145 160 155 160
 Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
 165 170 175
 Cys Leu Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
 180 185 190
 Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His
 195 200 205
 Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys
 210 215 220
 Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
 225 230 235 240
 Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
 245 250 255
 Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
 260 265 270
 Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
 275 280 285
 Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu
 290 295 300
 Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gln Gly Thr Cys
 305 310 315 320
 His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His
 325 330 335
 Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala
 340 345 350
 Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu
 355 360 365
 Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
 370 375

<210> 5
 <211> 1088
 <212> DNA
 <213> Rattus norvegicus

<400> 5

atggcccgga gaagagccctt ccctgttttc gggctccggc tttggggcat cctacatggc 60
 ctgcgtccatgc tacggcgaga tgcaggggcag ccggccaggaa agagctgtt cctgtggatc 120
 gacggccatc agggccagagt actccatggaa ttgtggaaag aatccatgtt tgctctggag 180
 ggaaataatgg ccccttttac atatgatttc agggaaatcc aatcaaaatgtt gccaggccatt 240
 cccgtcaata tccactccat gaaatttacc tggccaaatgtt caggccggc agagtttttc 300
 taatggatcc ttttgtttcc ttcgttgttggat aaaggccatca tggccatccc aatgtttcaat 360
 gtcctccggc tggggaaatgtt gcttcacaatg gcatcaatgtt ttcaatgtt tttccctggat 420

ctcgccaaac aggatggggg ggcagcattt gaaatgtat tgattgtcat gaattttgtaa 480
 ggcacccccca tccttcggac ccctcaaat getatctct ttaaaacaatg tcaacaatgt 540
 gagtgcccgag ggggtgtc aaatggggc ttttggaaac aaaggccgggt ctggcagtgt 600
 cccatgtggat tctatggacc tcaatgttag aaatgcctcg gatgtatgtaa 660
 ggtggctgt gtgtcacttc tggcttctgt atctgcctcg ctggatttca cgggttcaat 720
 tggatgtatggc caaatgttgc ggcacatgtc tttaatggg ggcacatgtt ttacccaggaa 780
 aaatgttattt ggcctccagg acttggggg gggcggatgt aatcagcaat gtgtttttcaat 840
 cccatgcggaa acgggggtaa atgcattttt aatggccatgt ctgttcgca gcttggatgtc 900
 ggtggcccaatg gaaatgtccaa cggacccaaat gatgttgcgt gtcgaggggg ctggatgtgg 960
 agacactgtca alaaatggta cggacccaaatc tcatgtatg cccggaggcc agcagggtcc 1020
 gggctggggc ggcacacggcc ttcaataaa aatggctggg ggcggaggaa tccacatgtaa 1080
 tccatataca tctgggtga 1098

<210> 6

<211> 365

<212> PRT

<213> Rattus norvegicus

<400> 6

Met Ala Arg Arg Ala Phe Pro Ala Phe Val Leu Arg Leu Trp Ser
 1 5 10 15Ile Leu Pro Cys Leu Leu Leu Arg Ala Asp Ala Gly Gin Pro Pro
 20 25 30Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gin Ala Arg Val Leu
 35 40 45Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
 50 55 60Pro Phe Thr His Asp Phe Arg Lys Ala Gin Gin Arg Met Pro Ala Ile
 65 70 75 80Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gin Ala Ser Gly Gin
 85 90 95Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
 100 105 110Ile Met Ala Asp Pro Thr Val Asn Val Pro Arg Leu Gly Thr Val Pro
 115 120 125His Lys Ala Ser Val Val Gin Val Gly Phe Pro Cys Leu Gly Lys Gin
 130 135 140Asp Gly Val Ala Ala Phe Glu Val Asn Val Ile Val Met Asn Ser Glu
 145 150 155 160Gly Asn Pro Ile Leu Arg Thr Pro Gin Asn Ala Ile Phe Phe Lys Thr
 165 170 175Cys Gin Gin Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
 180 185 190Asn Glu Arg Arg Val Cys Glu Cys Pro Asp Gly Phe Tyr Gly Pro His
 195 200 205Cys Glu Lys Ala Leu Cys Ile Pro Arg Cys Met Asn Gly Gly Leu Cys
 210 215 220Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
 225 230 235 240Cys Asp Lys Ala Asn Cys Ser Ala Thr Cys Phe Asn Gly Gly Thr Cys
 245 250 255Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Gly Glu Gin
 260 265 270Cys Glu Leu Ser Lys Cys Pro Gin Pro Cys Arg Asn Gly Gly Lys Cys
 275 280 285Ile Gly Lys Ser Lys Ser Val Cys Glu Pro Gly Cys Gly Ala His Gly
 290 295 300Thr Cys His Glu Pro Asn Lys Cys Gin Cys Arg Glu Gly Trp His Gly
 305 310 315 320

Arg His Cys Asn Lys Arg Tyr Gly Ala Ser Leu Met His Ala Pro Arg
325 330 335

Pro Ala Gly Ala Gly Leu Glu Arg His Thr Pro Ser Leu Lys Lys-Ala
340 345 350

Glu Gly Arg Arg Asp Pro Pro · Glu · Ser Asn Tyr Ile Trp
355 360 385

<210> 7
<211> 1125
<212> DNA
<213> *Xenopus* · sp.

〈400〉 7

〈210〉 8

{211} 374

{212} PRT

<213> Xenopus sp.

<400> 8

Met Ser Leu Thr Gly Tyr Phe Ala Ala Pro Leu Cys Ser Ile Phe Leu
1 5 . 10 . 15

Phe Ile Leu Ala His Ala Asp Ala Gly Gln Gln Glu Asp Ser Leu Tyr
20 25 30

Met Trp Ile Asp Ala His Gin Ala Arg Val Leu Ile Gly Phe Glu Glu
36 40 45

Asp Ile Leu Ile Val Ala Glu Gly Lys Met Ala Pro Phe Thr His Asp
50. 55 60

Phe Arg Lys Ala Gin Gin Arg Met Pro Ala Ile Pro Val Asn Ile His
85 70 75 80

Ala Met Asn Phe Thr Trp Gin Ala Thr Gly Gin Ala Glu Tyr Phe Tyr
85 90 95

Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly Ile Met Ala Asp Pro
100 105 110

Thr Val Asn Met Pro Leu Leu Gly Thr Val Pro His Lys Ala Thr Val
116 120 125

Ile Gin Val Gly Phe Pro Cys Leu-Gly Asn Gin Asp Gly Val Ala Ala
130 135 140

Phe Glu Val Asn Val Ile Val Met Asn Ser Glu Gly Asn Val Ile Leu
145 150 155 160

Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr Cys Gln Gln Ala Lys
165 170 175

Cys Thr Gly Gly Cys Arg Asn Gly Gly Phe Cys Asn Asp Arg His Val
180 185 190

Cys Glu Cys Pro Asp Gly Phe Tyr Gly Pro His Cys Glu Lys Ala Leu

195	200	205
Cys Met Pro Arg Cys Met Asn Gly Gly Leu Cys Val Thr Pro Gly Leu 210	215	220
Cys Ile Cys Pro Pro Gly Tyr Tyr Gly Ile Asn Cys Asp Lys Val Asn 225	230	235
Cys Thr Thr His Cys Leu Asn Gly Gly Thr Cys Phe Tyr Pro Gly Lys 245	250	255
Cys Ile Cys Pro Ser Gly Tyr Glu Gly Glu Gln Cys Glu Thr Ser Lys 260	265	270
Cys Gin Gln Pro Cys Arg Asn Gly Gly Lys Cys Ser Gly Lys Asn Lys 275	280	285
Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu Cys Ser Lys Pro Val 290	295	300
Cys Glu Pro Ser Cys Gly Ala His Gly Thr Cys Ile Glu Pro Asn Lys 305	310	315
Cys Gln Cys Lys Glu Gly Trp Asn Gly Arg Tyr Cys Asn Lys Lys Tyr 325	330	335
Gly Ser Asn Leu Met Asn Ala Leu Arg Pro Thr Gly Ser Arg Asn Arg 340	345	350
Gln His Thr Pro Ser Pro Lys Arg Thr Glu Asp Arg Gln Ala Leu Pro 355	360	365
Glu Ser Asn Tyr Ile Trp 370		

<210> 10
 <211> 378
 <212> PRT
 <213> Danio rerio

 <400> 10
 Met Ala Phe Arg Thr Pro Ala Val Gin Leu His Leu Lys Ala Cys Val
 1 5 10 15
 Leu Leu Leu Leu Gly Gly Leu Leu Glu Ala Ala Tyr Gin Glu Arg Gly
 20 25 30
 Thr Met Tyr Met Trp Ile Asp Ala Asn Gin Ala Arg Ile Leu Ile Gly
 35 40 45
 Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala Pro Phe
 50 55 60

Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile Pro Val
 65 70 76 80
 Asn Ile His His Val Asn Phe Thr Trp Gln Ala Thr Asp Gln Ala Glu
 85 90 95
 Tyr Phe Tyr Glu Phe Gln Thr Leu Arg Ser Leu Asp Lys Asp Ile Met
 100 105 110
 Asp Asp Pro Thr Val Asn Val Pro Leu Leu Gly Ser Val Pro His Lys
 115 120 125
 Ala Ser Val Val Gln Val Gly Phe Pro Cys Arg Gly Asp Gln Asp Gly
 130 135 140
 Val Ala Ala Phe Glu Val Thr Ile Leu Val Met Asp Ala Gly Gly Asn
 145 150 155 160
 Ile Ile Leu Arg Thr Pro His Asn Ala Ile Phe Phe Lys Thr Cys Gln
 165 170 175
 Arg Ala Lys Cys Pro Gly Gly Cys Arg Asn Gly Gly Tyr Cys Asn Glu
 180 185 190
 Arg Gln Val Cys Glu Cys Gln Asp Gly Phe Tyr Gly Val His Cys Glu
 195 200 205
 Lys Ala Leu Cys Ser Pro Arg Cys Leu Asn Gly Gly Leu Cys Met Ser
 210 215 220
 Pro Gly Val Cys Ile Cys Pro Pro Gly Tyr Phe Gly Ser Ser Cys Glu
 225 230 235 240
 Arg Ala Asn Cys Ser Thr Thr Cys Leu Asn Gly Gly Thr Cys Phe His
 245 250 255
 Pro Gly Lys Cys Ile Cys Ala Val Ser Phe Glu Gly Val Arg Cys Glu
 260 265 270
 Leu Ser Lys Cys Arg Gln Pro Cys Arg Asn Gly Gly Lys Cys Thr Gly
 275 280 285
 Arg Asn Lys Cys Lys Cys Ser Lys Gly Tyr His Gly Asp Leu Cys Ser
 290 295 300
 Lys Ala Val Cys Glu Pro Ser Cys Gly Ala His Gly Thr Cys Val Glu
 305 310 315 320
 Pro Asn Arg Cys Gln Cys Arg Glu Gly Trp His Gly Arg His Cys Asn
 325 330 335
 Lys Arg Phe Arg Gly Gly Val Ser Asn Ser Gln Arg Val Ser Pro Ser
 340 345 350
 Lys His Lys Ser Pro Ser Val Ala Ala Ala Lys Glu Ala Pro Glu Thr
 355 360 365
 Ser Gln Pro Ser Glu Thr Asn Tyr Val Val
 370 375

<210> 11
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Artificial Sequence

<400> 11
 tgyathtgyc cnccttggntw bwybcd

26

<210> 12
 <211> 28
 <212> DNA
 <213> Artificial Sequence

220

<223> Description of Artificial Sequence:Artificial Sequence .

regnetneen certenskrc angbcd

26

〈210〉 19

<211> 4817

<212> DNA

<213> Artificial Sequence

220

<223> Description of Artificial Sequence:pCAGGS 6xHis construct.

<400> 13

ttttaaatac	atctaaagta	tatacgatgt	aacttggtgt	gacagttaacc	aaatgtttat	3840
caggtaggca	cctatccatcg	cgatcgatgt	atttcgttca	tccatagtgt	ccgtactccc	3900
cgttgtgtgc	ataatctatcg	tacggggaggg	cttacccatc	ggccccagtg	ctgtcaatgt	3960
accgcgagac	ccacgcctac	ccgttccatga	tttatcatcgca	ataaaaaaccgc	caggccggaa	4020
ggccggatgc	atggatgtgc	ctgtcaactt	ttccggctcc	atccaggctca	ttatgttttg	4080
ccggaaatgc	agagtaatgt	gttcggccgt	ttatgttttg	cgcaacgttg	ttggccatgtc	4140
tacccggatc	gggggtgtac	gttcgtcggt	tgggtatggct	tcattcgtgt	ccgggttccca	4200
acgatcaagg	cgatgtttatc	gtatccccat	gttgcacaaa	aaggccgtta	gtccatgttgg	4260
ttccgtccat	gttgtccatgg	gtatgtttgc	cgccgtgtta	tcattcgtatgg	ttatggcage	4320
actgcataat	tcttttactg	tcatggccatc	cgttaatgtgc	ttttctgtgtc	cttgtgtggta	4380
cataacccaa	tcatttcgtat	aatatgtttat	gtggccgaccc	aggatgttctt	ggccggcgte	4440
aaatacgggt	aataccggcc	cataatcgac	aactttttaaa	gtgttcatca	ttggaaaaacg	4500
tttttcgggg	cgaaaaactct	caaggatctt	acgcgttgtt	atgttcagggt	cgatgtttacc	4560
cactcgatca	ccccaaatgt	cttcgtccatc	tttatctttt	acccagcggtt	cttgtgtgatc	4620
aaaaaacaggaa	aggccaaaaatg	ccgcaaaaaaa	gggaatatagg	ccgacacccga	aatgtttgtat	4680
actctatactc	tttttttttt	aatatattttt	aagcaatttat	ttagggttttt	gttttcgtatgg	4740
cggtatcacat	tttttttttt	ttttagaaaaaa	tttttttttttt	tttttttttttt	tttttttttttt	4800
ccggaaaaatgc	ccacccatgt					4817

<210> 14
<211> 1140
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificial Sequence

<400>	14	<pre> atggctcgga gaagacccctt cccgtgtttc ggctccggc tctggagcat ctacccttgc 60 ctactccctgc tgccggcgaa tgcaggccag ccacctgagg agacttgta cctgaggatc 120 gaccggccat aggettaggt gtcataaggaa ttgaaggaa accttctgtat tgctccggag 180 ggggaaatgg ccccccttgc acatgtttc aggaaggcc aaccatggat ccggcccaat 240 cttgtcaata tccactccat gaattttacc leggaagctg cggggggggc agaaatctc 300 tgccgggttc tgctctgtgg ctcccggat aaaggccatca tggcagatcc aactgtcaat 360 gtcccttgc tggyaacaatg ccctccatca gcatcgttgc ttcaatgtgg ttcccccgtt 420 ctcggaacat aagacgggtt agcagatctt gaaatgtttc ttatgttc ttatgttgc 480 ggcaacacca tcccttaggt ccctcgaaat ccacatcttcc tttaaaaaatc tcaacaatg 540 gaggtgtcccg gagggtgtcg aaatgggggc ttgtgtaaacg aaaggccgggt ctggaggtgt 600 ccggatgggt tctacgggaa tcactgtgg agggccctgt gcataccccg atgtatgaaat 660 gggtgttgc tgigcaccc tggcttctgc atctgcggccc ctggatctca cgggtgtcaat 720 ttgtacaaaat caaacatgc aaccacccgtc tttaatggag ggccctgttt ttaaccgggg 780 aaatgttattt ggccctccgtt actcgaggaa gggcgtgtg aactcageaa atggccccaas 840 ccctggccaa atgggggtaa atgcatttgtt aaaagccaaat gtaagtggccc gaaagggttac 900 caaggagacc tggtgtcttc gccccgtctgc gagecttgcgt gtggtgccta cggaaacctgc 960 caaaatggcc acaatgttca gtgtccggag ggctggccat gggacactgtt ctaataaggagg 1020 ttatggccca ggcctcatgg tggccgggg ccggccggcc tggggcttggaa gggccacacg 1080 cccttactta aaaaggctgtt ggatagaagg gatccatctg aatccatatta cattttgttgc 1140 </pre>
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<210> 15
<211> S79.
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificial Sequence

<400> 15
 Met Ala Arg Arg Arg Ala Phe Pro Ala Phe Ala Leu Arg Leu Trp Ser
 1 5 10 15
 Ile Leu Pro Cys Leu Leu Leu Arg Ala Asp Ala Gly Gln Pro Pro
 20 25 30
 Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
 35 40 45
 Ile Gly Phe Glu Glu Asp Leu Leu Ile Val Ser Glu Gly Lys Met Ala
 50 55 60
 Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
 65 70 75 80
 Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
 85 90 95
 Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly

	100	105	110
Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro			
115	120	125	
His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln			
130	135	140	
Asp Gly Val Ala Ala Phe Glu Val Asn Val Ile Val Met Asn Ser Glu			
145	150	155	160
Gly Asn Thr Ile Leu Arg Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr			
165	170	175	
Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys			
180	185	190	
Asn Glu Arg Arg Val Cys Glu Cys Pro Asp Gly Phe Tyr Gly Pro His			
195	200	205	
Cys Glu Lys Ala Leu Cys Ile Pro Arg Cys Met Asn Gly Gly Leu Cys			
210	215	220	
Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn			
225	230	235	240
Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys			
245	250	255	
Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln			
260	265	270	
Cys Glu Leu Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys			
275	280	285	
Ile Gly Lys Ser Lys Cys Lys Cys Pro Lys Gly Tyr Gln Gly Asp Leu			
290	295	300	
Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys			
305	310	315	320
His Glu Pro Asn Lys Cys Gln Cys Arg Glu Gly Trp His Gly Arg His			
325	330	335	
Cys Asn Lys Arg Tyr Gly Ala Ser Leu Met His Ala Pro Arg Pro Ala			
340	345	350	
Gly Ala Gly Leu Glu Arg His Thr Pro Ser Leu Lys Lys Ala Glu Asp			
355	360	365	
Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp			
370	375		

16
1140
DNB

213 Artificial Sequence

220

<223> Description of Artificial Sequence:Artificial Sequence

<400>.16

atggctcgga	gaagagccctt	ccctgttttc	gegcgtccggc	tctggaggcat	cetacccgtc	60
ctgtctctgtc	tgcgaggcgg	tgcaaggcgg	ccacttggaa	agagcttgta	cctgtggalc	120
gaccggccatc	aggcagliagt	gcfcatagga	tttggaaagaag	acatttgtat	tgtctcgagg	180
ggggaaaatgg	cccccttttc	acatcgatcc	aggaaaggctt	accaaaatgtt	cccagccatt	240
ccctgtcaata	tccatctcatc	gatttttacc	tggaaaggctt	cgggggcggc	ggaaataatcc	300
tacgugtccc	tgtctctgtc	ctccatgtat	aaaggccatc	tggcagatctt	acctgtccat	360
gtcccttgc	tggaaacagt	gccttcacaa	gcatacgtttt	ttaaagggttt	tttccctgtgt	420
ctcggaacat	aaggacgggt	ggcagatctt	gaatgtttat	tgattgtcat	gaattctgtaa	480
ccggaaacaca	tectttagac	cccttgcata	gccatctttt	ttaaaaatcg	tcaacaacgt	540
gagtgtcctc	gaggatgtat	aatgggggt	tttttttttt	aaaggccgggt	ttttttttttgt	600
ccggatgggt	tctacgggccc	tcacttgttt	aaaggccctgt	gcataccccc	atgtatgtaa	660
ggtgtgtctgt	gtgttcactcc	tggcttttgc	atctggcccc	ctggatctca	gggtgttcac	720
tgtgtacaaag	ccaaactgttc	aaccacgttc	tttaatgggg	ggactctgttt	ttaccccgaaa	780
aaatgttattt	cccttccctgg	atcgagggg	gagcgttgtt	aatttcgtttt	atggccccc	840
ccctgtccggaa	atggaggatgtt	atgcattttt	aaaggccatc	tttttttttt	aaagggtttac	900
ccaggagacc	tgtgtcttcc	gccccgttgc	gagctgttgtt	tttttttttt	ccggaaaccttc	960

cacgaacctca acaaatggcca gtgtcgagag gcttcggacg ccagacactg caataaagg 1020
 tatggagcca gcctcatgtc tgcccccagg ccagcaggcc cgggcgttga ggcacacactg 1080
 ctttacatca aaaaaggctg ggatagangg gatccacactg aatccaaatc catctggta 1140

<210> 17
 <211> 879
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Artificial Sequence

<400> 17
 Met Ala Arg Arg Ala Phe Pro Ala Phe Ala Leu Arg Leu Trp Ser
 1 5 10 15
 Ile Leu Pro Cys Leu Leu Leu Arg Ala Asp Ala Gly Gln Pro Pro
 20 25 30
 Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
 35 40 45
 Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
 50 55 60
 Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
 65 70 75 80
 Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
 85 90 95
 Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Ile Asp Lys Gly
 100 105 110
 Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
 115 120 125
 His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
 130 135 140
 Asp Gly Val Ala Ala Phe Glu Val Asn Val Ile Val Met Asn Ser Glu
 145 150 155 160
 Gly Asn Thr Ile Leu Arg Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
 165 170 175
 Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
 180 185 190
 Asn Glu Arg Arg Val Cys Glu Cys Pro Asp Gly Phe Tyr Gly Pro His
 185 200 205
 Cys Glu Lys Ala Leu Cys Ile Pro Arg Cys Met Asn Gly Gly Leu Cys
 210 215 220
 Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
 225 230 235 240
 Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
 245 250 255
 Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
 260 265 270
 Cys Glu Leu Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
 275 280 285
 Ile Gly Lys Ser Lys Cys Lys Cys Pro Lys Gly Tyr Gln Gly Asp Leu
 290 295 300
 Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
 305 310 315 320
 His Glu Pro Asn Lys Cys Gln Cys Arg Glu Gly Trp His Gly Arg His
 325 330 335
 Cys Asn Lys Arg Tyr Gly Ala Ser Leu Met His Ala Pro Arg Pro Ala
 340 345 350

Gly Ala Leu Glu Arg His Thr Pro Ser Leu Lys Lys Ala Glu Asp
 355 360 365

Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
 370 375

<210> 18
 <211> 1140

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificial Sequence

<400> 18

atggatcgga gaagagccct cccgttttc gtgcgtccggc tctggagcat ctacattgc 60
 ctgtatcgat tgccggcgaa tgcaggccggc ccacccggg agacccgttg cctggggatc 120
 gacggccatc aggcttagatgt gtcataaggta tttaaaggaa acatcttgcat tgcttcgggg 180
 88ttaaaatgg ccccccattac acatgttttcc agggaaagcc aaaaagaataa gccaggcatt 240
 ctgtcaata tccactccat gaatttttacc tggcaagctg cggggcgggc agaatacttc 300
 tacggatgtcc tgcgttcggat. aaaggatcta tggcagatcc aactgtcaat 360
 gtccctttgc tggaaacagt gtcataacaag gcatcgttg tcaatgttc ttccctgt 420
 ctggcaaac aagacgggggtt agcagccattt gaatgtatc tttatgtat gaatttcgtat 480
 gccaacacca tccttaggaa cccatcataat gccatcttc taaaacatcg tcaatcangt 540
 ggatgtccgg gagggatgtcg aaatggggc ttttgcataatc aaaggcggtt tggggatgtt 600
 cccatgtggat ttcacggggc tcaatgtcgaa aaaggatgtt gtcataccccg atgtatgaaat 660
 gatggatgtt gtttttttttgc atctgtccat tggatgttata cgggttcac 720
 tggatcataatc tttatgtatc aaccacatgtt tttatgtatc gggatgtttt tttatccggat 780
 aaatgtatatt gcccctctgg actcgaggaa gggatgtcg aactcgtatc atggccccc 840
 cccatgtggat atggatgtt gtttttttttgc aaaggatgtt gtaatgtccc gaaatgttat 900
 caaggatgtt tttatgtatc gggatgtt gtttttttttgc atggatgtccc cggatgtt 960
 caccatgttca acaatgttca gtttttttttgc atggatgtt gtttttttttgc caataatgtt 1020
 tatggatgtt gtcataatc tggatgtt gggatgtt gggatgtt gggatgtt gggatgtt 1080
 tttatgtatc aaaaaggatgtt gggatgtt gggatgtt gggatgtt gggatgtt gggatgtt 1140

<210> 19

<211> 379

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificial Sequence

<400> 19

Met Ala Arg Arg Arg Ala Phe Pro Ala Phe Ala Leu Arg Leu Trp Ser
 1 6 10 15

Ile Leu Pro Cys Leu Leu Leu Arg Ala Asp Ala Gly Gln Pro Pro
 20 25 30

Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
 35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
 50 55 60

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
 65 70 75 80

Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
 85 90 95

Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
 100 105 110

Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
 115 120 125

His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
 130 135 140

Asp Gly Val Ala Ala Phe Glu Val Asn Val Ile Val Met Asn Ser Glu
 145 150 155 160

Gly Asn Thr Ile Leu Arg Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr

165	170	175
Cys Gin Gin Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys		
180	185	190
Asn Glu Arg Arg Val Cys Glu Cys Pro Asp Gly Phe Tyr Gly Pro His		
195	200	205
Cys Glu Lys Ala Leu Cys Ile Pro Arg Cys Met Asn Gly Gly Leu Cys		
210	215	220
Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn		
225	230	240
Cys Asp Lys Val Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys.		
245	250	255
Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gin		
260	265	270
Cys Glu Leu Ser Lys Cys Pro Gin Pro Cys Arg Asn Gly Gly Lys Cys		
275	280	285
Ile Gly Lys Ser Lys Cys Lys Cys Pro Lys Gly Tyr Gin Gly Asp Leu		
290	295	300
Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys		
305	310	315
His Glu Pro Asn Lys Cys Gin Cys Arg Glu Gly Trp His Gly Arg His		
325	330	335
Cys Asn Lys Arg Tyr Gly Ala Ser Leu Met His Ala Pro Arg Pro Ala		
340	345	350
Gly Ala Gly Leu Glu Arg His Thr Pro Ser Leu Lys Lys Ala Glu Asp		
355	360	365
Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp		
370	375	

<210> 20
<211> 1140
<212> DNA
<213> Artificial Sequence

220> 223> Description of Artificial Sequence:Artificial Sequence

<400> 20						
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ctgtcttgc	tggaggggaa	tgcaggggag	ccactgtgggg	agagcttggta	cctgtggatc	120
gacggccatc	aggcttaggt	gtctatagga	tttgaaagaag	acatttcgtat	tgtctccggag	180
ggggaaatgg	ccccctttatc	acatgttttc	ggaaagaaggcc	aacanagaat	ggccaggccat	240
cctgtcaata	tccactccat	gaaatttacc	tggcaatgtcg	ccggggcgggc	agaatacttc	300
tatggatgtc	tgtctcttgtc	ctccccgtat	aaaggcatca	tggcagatcc	acttgtcaat	360
gtccctttgc	tggggacagt	gcctcaaca	gcataatgttg	tccaaatgg	tttccccgtgt	420
cctggaaaac	zaggacgggt	aggcggattt	gaagigaatg	tgttgttgc	gaatgttgc	480
ggccaaaccca	tccttagggc	cccttcggat	gccccatctt	ttaaaaaatg	tcacaaatgt	540
gagtgtcccg	gagggtgtcg	aaatggagge	ttttgttaacg	aaaaagggggt	ctgtcgagtgt	600
ccggatgggt	tctacggggc	tcactgttag	aaaaacccctgt	gcatacccccg	atgttatgtaa	660
ggtaggtgt	gtgtcacctc	tcgggttttc	atctcccccc	tggatgttca	cggtgtcaac	720
ttgtgatcaaa	aaaactgttc	aaaaacccgt	tttaatggag	ggacctgttt	tttccccggga	780
aaatgttattt	cccttcgg	actcgagggg	gatcgtgt	aacttcggaa	atcccccccaa	840
ccctgtccgg	atgggggtaa	atgcatttgt	aaaaggcaagt	gtaaatgtcccc	ggaaagggttat	900
caaggagacc	tgtgtcttca	gtttgttcgc	gagccclgggt	gttgtgtccca	ccggaaacctgc	960
caacggggcc	acaatgttca	gtgttcggag	ggcttggcagc	gtggacactgt	caataahagg	1020
tatggggcctc	gccttcatgc	tgtccccggg	ccggggatgtc	ttgggggtttca	ggccacacccg	1080
cccttcacttta	aaaagggtgt	ggatagaagg	gatccacccgt	aatccaatttgc	tatcttggtg	1140

<210> 21
<211> 379
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificial

Sequence

<400> 21
 Met Ala Arg Arg Arg Ala Phe Pro Ala Phe Ala Leu Arg Leu Trp Ser
 5 10 15
 Ile Leu Pro Cys Leu Leu Leu Arg Ala Asp Ala Gly Gln Pro Pro
 20 25 30
 Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
 35 40 45
 Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
 50 55 60
 Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
 65 70 75 80
 Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
 85 90 95
 Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
 100 105 110
 Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
 115 120 125
 His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
 130 135 140
 Asp Gly Val Ala Ala Phe Glu Val Asn Val Ile Val Met Asn Ser Glu
 145 150 155 160
 Gly Asn Thr Ile Leu Arg Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
 165 170 175
 Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
 180 185 190
 Asn Glu Arg Arg Val Cys Glu Cys Pro Asp Gly Phe Tyr Gly Pro His
 195 200 205
 Cys Glu Lys Ala Leu Cys Ile Pro Arg Cys Met Asn Gly Gly Leu Cys
 210 215 220
 Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
 225 230 235 240
 Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
 245 250 255
 Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Asp Gln
 260 265 270
 Cys Glu Leu Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
 275 280 285
 Ile Gly Lys Ser Lys Cys Lys Cys Pro Lys Gly Tyr Gln Gly Asp Leu
 290 295 300
 Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
 305 310 315 320
 His Glu Pro Asn Lys Cys Gln Cys Arg Glu Gly Trp His Gly Arg His
 325 330 335 340
 Cys Asn Lys Arg Tyr Gly Ala Ser Leu Met His Ala Pro Arg Pro Ala
 340 345 350
 Gly Ala Gly Leu Glu Arg His Thr Pro Ser Leu Lys Lys Ala Glu Asp
 355 360 365
 Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
 370 375

<210> 22
 <211> 558
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificial Sequence

<400> 22

atggctcgga gaagggcctt ccctgttttc ggcgtccggc tctggagcat cctacccgtc 60
 ctgtttccgtc tgccggcggg tgcggggcag ccacctgggg agagcttgta cctgtggatc 120
 gatggcccaatc aggcttaggt gctcatagaa ttgttggaaatc acatctgtat tggttggagg 180
 gggaaatgg cccccctttac acatgttttc agggaaagccc ttatggatc gccggccatt 240
 ctgttcaata tccatccatc gaatttttcc tggcaatgtg cggggccggc agaatatcc 300
 tacgggttcc tggctctgtcg ctccatggatc aaagggtatc tggcagatcc aacttgtatc 360
 gtccctttgc tggggacatgt ggcttacang gcatcgttgg ttcaatgttgg 420
 ctggcaaac aegacgggggtt agggatgtt gaaatgtatc tgatgtatc gaatgtatc 480
 gggaaatccatc tccatggatc cccatgtatc ttatggatc gctggccat 540
 ctatcatatc atcattgtc 558

<210> 23

<211> 185

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificial Sequence.

<400> 23

Met Ala Arg Arg Arg Ala Phe Pro Ala Phe Ala Leu Arg Leu Trp Ser
 5 10 15

Ile Leu Pro Cys Leu Leu Leu Arg Ala Asp Ala Gly Gln Pro Pro
 20 25 30

Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
 35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
 50 55 60

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
 65 70 75 80

Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
 85 90 95

Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
 100 105 110

Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
 115 120 125

His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
 130 135 140

Asp Gly Val Ala Ala Phe Glu Val Asn Val Ile Val Met Asn Ser Glu
 145 150 155 160

Gly Asn Thr Ile Leu Arg Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
 165 170 175

Gln Leu Ala His His His His His His
 180 185

<210> 24

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificial Sequence

<400> 24

atggctcgga gaagggcctt ccctgttttc ggcgtccggc tctggagcat cctacccgtc 60
 ctgtttccgtc tgccggcggg tgcggggcag ccacctgggg agagcttgta cctgtggatc 120
 ttgttcaatc aaaggccgggt ctggcgtgttggatc cggggatgttggatc tcaatgttgg 180
 aaacccgtt gcatatccatc atgtatgtac ggtgggtgttggatcactcc tggcttctgc 240
 atctggccatc ctggattcta cgggtcaac tctggatcggg cttactgtc aaccacccgtc 300

tttaatggag ggacctgttt ttacccggga aaatgttattt gcccctctgg actcgaggga 350
 gagcagtgtg aaccicageaa atgcgcccaa cctgcgcgaa atgggggtaa atgcatttgtt 420
 aaaaaggcaatgttgcctt gaaagggtac caaggagacc tggcgtctaa gcccgttgtc 480
 gagecctggctt tggtggccca cggancctgc cacggaccca acaatgtcca gtgtcgagag 540
 ggctggcactg caataaggaa tggggatca ecctcatgca tgccccgggg 600
 ccacggggcg cggggctggaa gggacacacg ctttactta aaaaggtga ggatagagg 660
 gatccacccgt aatccattt catctggcag ctggccatc atccatcatca tcatttg 717

<210> 25

<211> 238

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificial Sequence

<400> 25

Met Ala Arg Arg Arg Ala Phe Pro Ala Phe Ala Leu Arg Leu Trp Ser
 1 5 10 15Ile Leu Pro Cys Leu Leu Leu Leu Asp Cys Gln Gln Ala Glu Cys
 20 25 30Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys Asn Glu Arg Arg Val Cys
 35 40 45Glu Cys Pro Asp Gly Phe Tyr Gly Pro His Cys Glu Lys Ala Leu Cys
 50 55 60Ile Pro Arg Cys Met Asn Gly Gly Leu Cys Val Thr Pro Gly Phe Cys
 65 70 75 80Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn Cys Asp Lys Ala Asn Cys
 85 90 95Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys Phe Tyr Pro Gly Lys Cys
 100 105 110Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln Cys Glu Leu Ser Lys Cys
 115 120 125Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys Ile Gly Lys Ser Lys Cys
 130 135 140Lys Cys Pro Lys Gly Tyr Gln Gly Asp Leu Cys Ser Lys Pro Val Cys
 145 150 155 160Glu Pro Gly Cys Gly Ala His Gly Thr Cys His Glu Pro Asn Lys Cys
 165 170 175Gln Cys Arg Glu Gly Trp His Gly Arg His Cys Asn Lys Arg Tyr Gly
 180 185 190Ala Ser Leu Met His Ala Pro Arg Pro Ala Gly Ala Gly Leu Glu Arg
 195 200 205His Thr Pro Ser Leu Lys Lys Ala Glu Asp Arg Arg Asp Pro Pro Glu
 210 215 220Ser Asn Tyr Ile Trp Gln Leu Ala His His His His His His His
 225 230 235